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18-08-301-20/-/4.m

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OM nucleic - nucleic search, using sw model

June 4, 2004, 08:34:44; Search time 65 Seconds (without alignments) 2868.669 Million cell updates/sec

Run on:

US-09-301-507-74 336 1 CGCTGCATCTTTTCTATGC......CCCCNTTGGTTCCCAACCCA 336 Title: Perfect score:

Sequence:

IDENTITY NUC Gapext 1.0

Scoring table:

682709 segs, 277475446 residues Searched:

1365418 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	App	Ap.	Ap	Ap	Αp	Ap	Αp	Ap	7, App	pli	ppl	pli	pli	pli	ppl	ppl	o, App	App	pli	Ap	pli	pli	Appli	pli	Ap	Appl	Ą
ជ	625,	··i		-			9249,	64	42	7	13	3, Ap	5, Ap	7, Ap		17	33	35	æ,	61	Ä	H	2, Ap	2, Ap	1483,		14464
Description	Sequence	Seguence	Sequence	Sequence	Seguence	Seguence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence
QI	US-09-620-312D-625	-09-252	-09-252	-09-621-	-09-252-991A-870	-09-252-	US-09-252-991A-9249	-09-489-039A-64	US-09-620-312D-427	338-151A	-08-83	38-838-151A-	US-08-838-151A-5	-80	US-08-838-151A-15	US-08-838-151A-17	US-09-620-312D-330	US-09-620-312D-353	US-09-740-027-3	US-09-833-381-1969	US-08-793-273C-1	11684-	98-35	-08	-010-60-	-008-60-	US-09-621-976-14464
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Gaps

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Query Match

23.5%; Score 78.8; DB 4; Length 1878;
Best Local Similarity 87.8%; Pred. No. 7.6e-19;
Matches 108; Conservative 0; Mismatches 13; Indels 2.

Sequence 1, Appli Sequence 11175, A Sequence 11, Appli Sequence 2, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli	
US-09-214-808-1 US-09-621-976-11175 US-09-976-11175 US-09-976-111 US-09-103-840A-2 US-09-103-840A-1 US-09-113-840A-1 US-09-113-840A-1 US-09-116-340A-1 US-09-116-340A-3 US-09-211-710-3 US-09-615-192A-3 US-09-615-192A-3 US-09-615-192A-3 US-09-479-409-6 US-09-479-409-6 US-09-479-409-6 US-09-479-409-6 US-09-479-409-6 US-09-479-409-6	US-09-169-789-124 US-08-975-316-48
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ALIGNMENTS

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APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Dannac, Radoje T.
APPLICANT: Dramanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: NO. 90406620, 312D
CURRENT APPLICATION NUMBER: US/09/620, 312D
CURRENT FILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PLF_Genes Version 1.0
SEQ ID NO 625
LENGTH: 1878
sequence 625, Application US/09620312D
                                                                                                                                                                        Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
                                                                     APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
                                                                                                                                                                                                                                                        Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunqing
Wang, Dunrui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (945)..(1229)
US-09-620-312D-625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
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95 GCGNCTGCATGAGGCACCACTATGTTGNATTCTATCAGCTCACCCGTTGNTACAAGTGTA 154
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               Query Match
9.1%; Score 30.6; DB 4; Length 3:
Best Local Similarity 45.0%; Pred. No. 0.8;
Matches 90; Conservative 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 CNCATGGCAGTCCTTGGNCA 294
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US-09-252-991A-8705/c
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US-09-621-976-2911
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Matches 62,
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Sequence 4491, Application US/09252991A

Sequence 4491, Application US/09252991A

Sequence 4491, Application US/09252991A

Sequence 4491, Application US/09252991A

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOWONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 651
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APPLICANT: NO. 0231737
APPLICANT: NO. 0231737
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4398
LENGTH: 3105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 ecescicarricceccaccecesaescricecricarcarcarcarcarcaccececcarcece 309
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                                                    524 gacadericar-rearangaaeregaaceeregaege-ergeargaggereererangig
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9.1%; Score 30.6; DB 4; Length 651;
Best Local Similarity 45.0%; Pred. No. 0.32;
Matches 90; Conservative 0; Mismatches 110; Indels
62 GACAGCTCGINTCAIGAICGACTCGGACCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.09-252-991A-4398/c
Sequence 4398, Application US/09252991A
Patent No. 6551795
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US-09-252-991A-4491
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US-09-252-991A-4398
                                                                                                               122 NAT 124
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Sequence 8705, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: A LINFORMATION:
TITLE OF INVENTION: ACCIDENCE ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRESENCE: 107196.138
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 AGGGNCCTGGTCGTCCCATCGCCTAGCAGGGTTCAAGNAAAGGGGCCCGCNCATGGCAGT 285
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US-09-6211/C
US-09-6211, Application US/09621976
; Sequence 2911, Application US/09621976
; Patent No. 6639063
; GENERAL INPORMATION:
; APPLICANT: Undert, S.
; APPLICANT: Jobert, S.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; CURRENT APPLICATION UNMERS: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SEQ ID NO 2911
LENGTH: 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.0%; Score 30.2; DB 4;
Local Similarity 51.2%; Pred. No. 0.4;
Les 62; Conservative 0; Mismatches 59;
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ORGANISM: Homo sapiens
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/469,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 6423
LENGTH: 1281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 TGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCTGAGNTTCCAGAGGGNCC
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Pred. No. 0.95;
0; Mismatches 101; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.9%; Score 30; DB 4; Length 1293; Best Local Similarity 54.5%; Pred. No. 0.8; Matches 54; Conservative 0; Mismatches 45; Indels
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; Sequence 6423, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
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                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6423
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Best Local Similarity 45.7%;
Matches 85; Conservative
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Peiyan
APPLICANT: Chen, Rai-hong
PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 9249
LENGTH: 1293
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Sequence 9076, Application US/09252991A
Parent No. 6551795
GENERAL INFORMATION:
TATLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERCIGNOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9249, Application US/09252991A

Sequence 9249, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/04,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 4; Length 1080;
Pred. No. 0.72;
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9076
                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8705
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il Similarity 54.5%;
54; Conservative
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Matches 54; Conserv
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Best Local Similarity
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US-09-252-991A-9076
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us-09-301-507-74.rni

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ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/838,151A
                                                                                                                        APPLICATION NUMBER: US/08/838,1517
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mealler, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801POZ-
TELEPHONE: 312-616-5400
ITELEPHONE: 312-616-5400
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE GHARATERISTICS:
LENGTH: 1166 base pairs
TYPE: nucleic acid
STRANDEDRES: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ONIGINAL SOURCE:
ORGANISM: Tomato Mottle Geminivirus
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME:FREV.
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; LOCATION: 44..436
US-08-838-151A-13
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8.8%; Score 29.6; DB 3; Length 1166;
Best Local Similarity 63.1%; Pred. No. 1.1;
Matches 41; Conservative 0; Mismatches 24; Indels 0. 265 AAGGG 269

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724 CAGGG 728

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Sequence 3, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Luu, Hang T

APPLICANT: Hangon, Steve

TITLE OF INVENTION: Genes

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSE: ADDRESS:

ADDRESSE: ADDRESS:

ADDRESSE: ADDRESS:

CONTRES Illinois

CONTRES ILLinois

COMPUTER: ILLinois

COMPUTER: ELOPPY disk

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

Query Match
8.8%; Score 29.6; DB 3; Length 1169;
Best Local Similarity 63.1%; Pred. No. 1.1;
Matches 41; Conservative 0; Mismatches 24; Indels 0

720 CAGGG 724 셤

265 AAGGG 269

sequence 5, Application US/08838151A

Sequence 5, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:
APPLICANT: Baxwell, Douglas
APPLICANT: Maxwell, Douglas
APPLICANT: Maxwell, Douglas
APPLICANT: Hanson, Steve
ITITLE OF INVENTION: Genes
ITITLE OF INVENTION: Genes
ITITLE OF INVENTION: Genes
INUMBER OF SEQUENCES: Genes
STREET: Two Prudential Plaza, Suite 4700

STREET: Two Prudential Plaza, Suite 4700

STREET: Illinis
COUNTRY: U.S.A.

ZIP: 60601

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible RESULT 13 US-08-838-151A-5

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| Sequence 7, Application US/08838151A
| Sequence 7, Application US/08838151A
| Patent No. 629143
| Patent No. 629143
| APPLICANT: Stout, John T
| APPLICANT: Maxwell, Douglas
| APPLICANT: Hangs
| APPLICANT: Hangson, Steve
| TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
| TITLE OF INVENTION: Genes
| TITLE OF INVEN
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8.8%; Score 29.6; DB 3; Length 1169;
Best Local Similarity 63.1%; Pred. No. 1.1;
Matches 41; Conservative 0; Mismatches 24; Indels 0.
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: circular
TOPOLOGY: circular
HYDCHEFICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANIEN Tomato Mottle Gemini Virus
STRAIN: Florida
SOFTWARE: Patentin Release #1.0, Vocurrent Application Data:
Application NUMBER: US/08/838,151A
                                                                                                        FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INVERMATION:
NAME: MAGLIEr, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SV33E
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-616-5400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 base pairs
TYPE: nucleic acid
STRANDENESS: single
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CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 44..1127
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US-08-838-151A-5
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RESIDENCENTOR NUMBER: 18,978
RESERRENCE DOCKET THREER: 18,978
RESIDENCENTOR NUMBER: 18,978
RESIDENCED THREE OF THREE RESIDENCES
RESIDENCES: 132-66-540
RESIDENCE
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SEQUENCE CHARACTERISTICS:
LENGTH: 1246 base pairs
TYPE: nucleic acid
STRANDENESS: single
STRANDENESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Geminivirus
STRAIN: Florida
PUBLICATION INPORMATION:
AUTHORS: Hidavat, SH
AUTHORS: Hidavat, SH
AUTHORS: Paplomatas, EJ
AUTHORS: Paplomatas, EJ
AUTHORS: Maxwell, DP
TITLE: Pseudorecombination between the infectious
TITLE: dwarf mosaic geminiviruses.
JOURNAL: Journal of General Virology
VOLUME: 74
PAGES: 23-31
BATE: 1993
US-08-838-151A-15
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Search completed: June 4, 2004, 15:49:56 Job time: 72 secs

265 AAGGG 269 ||||| 317 CAGGG 321

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Query Match 8.8%; Score 29.6; DB 3; Length 1246; Best Local Similarity 63.1%; Pred. No. 1.1; Matches 41; Conservative 0; Mismatches 24; Indels 0; Gaps

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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- nucleic search, using sw model OM nucleic

June 4, 2004, 14:59:34; Search time 292 Seconds (without alignments) 5249.420 Million cell updates/sec US-09-301-507-74

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Run

336 1 CGCTGCATCTTTTCTATGC......CCCCNTTGGTTCCCAACCCA 336 Title: Perfect score:

Sequence:

IDENTITY NUC Gapopt 10.0 Scoring table:

Total number of hits satisfying chosen parameters:

2995936 seqs, 2280998010 residues

Searched:

5991872

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Query Match Learth to In Description	Macon Bengul DB 1D	318 94.6 336 16 US-10-355-716-74 Seguence 74, Appl	6.8 25.8 252 16 US-10-355-716-76 Sequence 76, Appl	9.8 23.8 412 15 US-10-198-846-1775 Sequence 1775, Ap	8.8 23.5 455 15 US-10-198-846-8657 Seguence 8657, Ap	23.5 1878 15 US-10-037-270-625 Sequence	23.5 1878 16 US-10-117-722-625 Sequence	78.8 23.5 2061 15 US-10-198-846-11013 Sequence 11013, A	10.2 254087 13	9.7 2464 13 US-10-424-599-123456	9.6 23715 13	9.5 368 13 US-10-424-599-2667 Sequence	9.4 2181 17 US-10-380-040A-7 Sequence 7, A	9.4 96596 12 US-09-997-722-196 Sequence
æ		- 1	8 94.6	8 25.8	8 23.8	8 23.5									
	Result		1 31	2 86.	3 79.	4 78.	5 78.	6 78.	7 78.	8 34.	9 32.		11 31.		13 31.
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Sequence 15342, A

US-09-918-995-15342

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9.3

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Sequence 506, Applia Sequence 4, Applia Sequence 20635, Applia Sequence 27153, A Sequence 27153, A Sequence 307934, Sequence 307936, Sequence 307936, Sequence 273, Applia Sequence 111, Applia Sequence 16994, Sequence 19694, Sequence 19694, Sequence 264399, Sequence 45, Applia Sequence 46, Applia Sequence 11, Applia Sequence 11, Applia Sequence 45, Applia Sequence 45, Applia Sequence 14, Applia Sequence 11, Applia	
US-10-044-090-506 US-09-079-892-4 US-10-08-44-060-685 US-09-864-761-20635 US-09-864-761-2053 US-10-087-192-259 US-10-087-192-259 US-10-027-632-307936 US-10-027-632-307936 US-10-027-632-307936 US-10-027-632-307936 US-10-027-632-307936 US-10-027-632-307936 US-10-027-632-307936 US-10-027-632-307936 US-10-25-068-77 US-10-25-068-77 US-10-25-068-77 US-10-29-96803 US-10-027-632-264399	
1053 30023 30023 267 267 267 267 267 267 267 267 267 267	
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ALIGNMENTS

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NUMBER OF SEQUENCES: 132

CORRESPONDENCE ADDRESS:

ADDRESSES: 36ed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: 102
COMPUTER: READABLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: 18D PC COMPATIBLE
COMPUTER: 18D PC CKET NUMBER: 23 0018,401C1
TELECOMUNICATION INPORMATION:
T
                                                                                                           Sequence 74, Application US/10355716
Publication No. US200316339A1
GENERAL INFORMATION:
APPLICANT: Cynader, Max
APPLICANT: Cynader, Max
TITLE OF INVENTION: PLASTICITY AND METHODS RELATED THERETO
RESULT 1
US-10-355-716-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCTGAGNTTCCAGAGGGNCTGGTCGTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GGACAGCTCGTNTCATGATCGACTCGGACCCTCTGCGNCTGCATGAGGCACCACTATGTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 CCATCGCCTAGCAGGGTTCCAAGNAAAGGGGCCCGCNCATGGCAGTCCTTGGNCAGNAGNA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGACAGCTCGTNTCATGATCGACTCGGACCCTCTGCGNCTGCATGAGGCACCACTATGTT
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US-10-355-716-76
; Sequence 76, Application US/10355716
; Publication No. US20030216339A1
; GENERAL INFORMATION:
; APPLICANT: Cynader, Max
; APPLICANT: Cynader, Max
; TITLE OF INVENTION: GENE SEQUENCES ASSOCIATED WITH NEURAL
; TITLE OF INVENTION: GENERAL PLASTICITY AND METHODS RELATED THERETO
; NUMBER OF SEQUENCES: 132
; TOTAL OF SEQUENCES: 132
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ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                      Query Match 94.6%; Score 318; DB 16; Length 336; Best Local Similarity 100.0%; Pred. No. 5e-108; Matches 336; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: FLOPDY disk
COMPUTER: 1BM PC compatible
COMPUTER: DATE: PLOPDY disk
COMPUTER: DATE: PLOPDY disk
COMPUTER: DATE: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: <a href="https://doi.org/10/355/716">CLASSIFICATION: <a href="https://doi.org/10/355/716">ADDATA: <a href=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 ANGGANTIGGNCCCAACCCCNITGGTTCCCAACCCA 336
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REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 230018.401C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/301,507
FILING DATE: 28-Apr-1999
ATTORNEY/AGENT INPORMATION:
                                                                                                                                           TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
                                       LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
STATE: Washington
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APPLICANT: Lilité, James
APPLICANT: Wangy Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILLE REPERENCE: MRI-049
CURRENT APPLICATION NUMBER: 105/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR PILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE FEAST FRANCE FRANCE
SEQ ID NO 1775
LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 COCTOCATCTTTTTCTATGCTCTCCTGCTGGCGCTGATGGGAGATACAGACAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGACAGCTCGTNTCATGATCGACTCGGACCC
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHRAACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 76:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-10-198-846-8657
Sequence 8657, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-198-846-1775
; Sequence 1775, Application US/10198846
; Publication No. US20030099974A1
; GRNERAL INFORMATION:
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) LOCATION: 3, 203, 293, 343, 398
) OTHER INFORMATION: n = A,T,C or G
US-10-198-846-1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GNAT 124
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SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 625
LENGTH: 1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (945)..(1229)
US-10-117-722-625
                                                                                                                                       ; NAME/KBY: CDS
; LOCATION: (945)..(1229)
US-10-037-270-625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 NAT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  582 ATT 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 GACAGCTICAT-TICATAATGGACTICGGACGTICGACG-CTGCATGAGGCACCACTATGTGG 177
                      APPLICANT: Xu, Yongvao

APPLICANT: Xu, Yongvao

APPLICANT: Steinmann, Kathleen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

TITLE OF INVENTION: THERAPY OF BREAST CANCER

TITLE OF INVENTION: THERAPY OF BREAST CANCER

FILE REFERENCE: MILO49

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: PASTER OF SEQ for Windows Version 4.0

SEQ ID NO 8657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT PILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.5%; Score 78.8; DB 15; Length Best Local Similarity 87.8%; Pred. No. 1.3e-18; Matches 108; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 625, Application US/10037270
Publication No. US20030104529A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Anng, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Chang, Oing A.
APPLICANT: Chang, Oing A.
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Duntui
                                                                                                                                                                                                                                                                                                                                                                                                                                              | NAME/KEY: misc_feature
| LCCATION: 2, 7, 404, 454
| CTHER INFORMATION: n = A,T,C or G
| US-10-198-846-8657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GCTGCATCTTTTTCTATGC
APPLICANT: Lillie, James
                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 ATT 180
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APPLICANT:
APPLICANT:
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62 GACAGCTCGTNTCATGATCGACTCGGACCCTCTGCGNCTGCATGAGGGACCACTATGTTG 121
                                                                                                                                                                       464 ściecarceririczarecrerecenscrearanareceasaracasacasaranas 523
                                                                                                                                                                                                                                                                  524 GACAGCTCAT-TCATAATGAACTCGAACCCTCGACG-CTGCATGAGGCACCACTATGTGG 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 GACAGCTCGTNTCATGATCGACTCGGACCCTCTGCGNCTGCATGAGGCACCACTATGTTG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GCTGCATCTTTTCTATGCTCTCCTGCTGGCGCTGATGGGGAGATACAGACAAAACG
                                                                                                                      Gaps
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      Length 1878;
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Sequence 625, Application US/10117722
Publication No. U520030219744A1
GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Talu, Chenghua

APPLICANT: Asundi, Vinod

TITLE OF INVENTION: No. U520030219744A1e1 Nucleic Acids and

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 784CIP2BCIP

CURRENT APPLICATION NUMBER: 08/10/117,722

CURRENT APPLICATION NUMBER: 09/520,312

PRIOR FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1104

SOFTWARE: PLEGENES VETSION 1.0

SEQ ID NO 625

LENGTH: 1878
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                                                            Indela
Query Match
23.5%; Score 78.8; DB 15;
Best Local Similarity 87.8%; Pred. No. 2.5e-18;
Matches 108; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.5%; Score 78.8; DB 16; Best Local Similarity 87.8%; Pred. No. 2.5e-18; Matches 108; Conservative 0; Mismatches 13;
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427 GCTGCATCCTTTTCTAIGCTCTCCCTGCTGGTGATAATGGGAGATACAGACAGTAAAACG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GACAGCTCGTNTCATGATCGACTCGGACCTTGCGNCTGCATGAGGCACCACTATGTTG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GCTGCATCTTTTTCTATGCTCTCCTGCTGGCGCTGATGGGAGATACAGACAAAACG 61
Sequence 11013. Application US/10198846

Publication No. US20030099974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Lillie, James

APPLICANT: Lillie, James

APPLICANT: Wang, Youzhen

APPLICANT: WANGER: US/10/198,846

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT APPLICATION NUMBER: US/10/198,846

FRIOR APPLICATION NUMBER: 60/306,220

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11013

LENGTH: DATE: 2061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAMENT/KEY: misc_feature
LOCATION: 1, 2, 3, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838,
LOCATION: 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846, 1847, 1848,
LOCATION: 1849, 1850, 1851, 1852, 1854, 1855, 1856, 1860, 2009,
LOCATION: 2039, 2041, 2042, 2043, 2044, 2045, 2046, 2047
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: 2064, 2069, 2051, 2052, 2053, 2054, 2055, 2056, 2057,
LOCATION: 2058, 2059, 2060, 2061
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11013
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23.5%; Score 78.8; DB 15; Length 2061;
Best Local Similarity 87.8%; Pred. No. 2.6e-18;
Matches 108; Conservative 0; Mismatches 13; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 223, Application US/10087192
Fublication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Mortis, David W.
APPLICANT: Engelhard, Eric K.
TILLE OF INVENTION: CANCER
TILLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR PLING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo Bapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                545 ATT 547
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Sequence 123456, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
FILE REFERENCE:
TITLE OF INVENTION:
FILE REFERENCE:
GURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE:
CURRENT FILING DATE:
MUMBER:
WUMBER:
SEQ ID NOS: 285684
SEQ ID NO 123456
SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                         34592 AAGTGATGACGCAAAAGGCAGTGACTGGGAGCCACTTTATTTTTTATTATATCTCAG 34651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 AAGTGTAGNCTCAAAGGAAGAATAGTGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 TCACCCGTTGNTACAAGTGTAGNCTCAAAGGAAGAATAGTGGGGAGTCTTCTGTGAGACCT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 Tranciccadaceccacceccaccacadadaadaadaadaadadagadaccidadrace 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 NTGGCCCTGAGNTTCCAGAGGGNCCTGGTCGTCCCATCGCCTAGCAGGGTTCAAGNAAAG 267
                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                             Length 254087;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 ACTAACTCCGCGGATGGCGCCGAATCTCGACAGGCACCTTGTGTTCCC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2464;
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                                                                                                                                                                                                                                                                                                                                                 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.7%; Score 32.6; DB 13;
Best Local Similarity 54.1%; Pred. No. 0.5;
Matches 59; Conservative 0; Mismatches 50;
                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Clone ID: PAT_MRT3847_82489C.1 US-10-424-599-123456
                                                                                                                                                                                                                                                                                             Query Match
10.2%; Score 34.4; DE
Best Local Similarity 51.9%; Pred. No. 0.8;
Matches 68; Conservative 0; Mismatches
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 223
LENGTH: 254087
TYPE: DNA
CRANISM: Mus musculus
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                                                                                                                                              FRATURE:
| NAME/KEY: misc_feature|
| LOCATION: (1)...(254087)
| COTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34712 ATGACAGAGCA 34722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 GGGCCCGCNCA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-123456
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US-10-087-192-1420
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Sequence 7, Application US/10380040A
Publication No. US20040077043A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: A NOVEL DENDRITIC CELL MEMBRANE MOLECULE AND USE THEREOF
TILE REPERENCE: PH-1297PCT-US
CURRENT FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: UP 2000-277352
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
TENNING. 210-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1329 CCTGCGGGTGGTGGTGGGGGATGGCACCTACAGCTGCTGCTGCGCACCCGTGCT 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1389 GCAGCAGGATGCGCACGGCTCTGTCACCATCACAGGGCAGCCTATGACATTCCCCCCAGA 1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1449 GTCTAĞAĞCAĞACTACAAĞĞACĞACĞATĞACTAĞAÇTAĞTĞACAAAACTCACACATGCCC 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 CGGACCCTCTGCGNCTGCATGAGGCACCACTATGTTGNATTCTATCAGCTCACCCGTTGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 CCTGCTGGCGCTGATGGGAGATACAGAACAGCAAAACGGACAGCTCGTNTCATGATCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 TACAAGTGTAGNCTCAAAGGAAGAATAGTGGGAGTCTTCTGTGAGACCTATCTGAATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Description of Artificial Sequence: a fusion OTHER INFORMATION: protein of BRIGHT extracellular domain (29-465); CTHER INFORMATION: and human IgGIFc domain US-10-380-0460A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

9.4%; Score 31.6; DB 17; Length
Best Local Similarity 46.6%; Pred. No. 1.1;
Matches 88; Conservative 0; Mismatches 101; Indels
             286 ACAGGCACCTTGTGTTCCC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1509 ACCGTGCCC 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 CGNNTGGCC 213
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; ORGANISM: Homo sapiens
US-09-997-722-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2181
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ear Rosa Thomas J
APPLICANT: Ear Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE APLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 2667
LENGTH: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1250 CIGGAGATITIAAACACATAACACTACTGCCAGCTTITIGGGGCTATITICTTAGTATIG 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1310 dénaggérernaggérarchagarnéhagéragrandarérrérrérrérrérréren 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1370 GTGAGAGGCCAAGAATAGCAGTGGACTTCCCAGAGATTGAGTCCAATCTAGGAATGAGTA 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 GNCTCAAAGGAAGAATAGTGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 GAAGAAGAAGAAGAAGAAGTGGTGGTAGGAGCTAGCTGCGGGGAATCTCG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 CTGATGGGAGATACAGACAGCAAAACGGACAGCTCGTNTCATGATCGACTCGGACCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 GCGNCTGCATGAGGCACCACTATGTTGNATTCTATCAGCTCACCCGTTGNTACAAGTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 23715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.5%; Score 31.8; DB 13; Length 368; Best Local Similarity 60.8%; Pred. No. 0.44; Matches 48; Conservative 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32.4; DB 13; Length Pred. No. 1.6; 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_102413C.1
US-10-424-599-2667
FILLE OF INVENTION: CANCER
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US/10/087,192
FRIOR APPLICATION NUMBER: US 09/747,377
FRIOR FILLING DATE: 2000-12-22
FRIOR FILLING DATE: 2001-22
NUMBER OF SEQ ID NOS: 2059
SOFTWARER: PASISEQ for Windows Version 4.0
SEQ ID NO 1420
LENGTH: 23715
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                                                                                                                                                                                                                                                                                                                                                                                                                   ) LOCATION: (1)...(23715)
) OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 45.8%;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Glycine max
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80951 CTATTATTAGGAAAGTGTGAGTCTGAATCTTTTCCCGTTGAATTTTAGTGTTTTAAAA 80892
                                                                                                                                          81011 GGAAAAACTTTGCCTTAAACAAATTTCTCACAATATGTACAATCATCTACCAAAGAGGTC 80952
                                                                                                                                                                                                                                                                                                                                                                                                 80891 GTGATCTGCAAGACACATGTTCTTTATTAGCTTAAAAAAGGGAGCCCTCTGCTGGTAGAA 80832
                                                                                                                                                                                                                                                                                                                                       227 GGGNCCTGGTCGTCCCATCGCCTAGCAGGGTTCAAGNAAAGGGCCCGCCACTCGCAGTC 286
                                                                                         107 GGCACCACTATGTTGNATTCTATCAGCTCACCCGTTGNTACAAGTGTAGNCTCAAAGGAA 166
                                                                                                                                                                                                                167 GAATAGTGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGGNNTGGCCCTGAGNTTCCAGA
                                         0; Gaps
Best Local Similarity 44.1%; Pred. No. 5.8;
Matches 94; Conservative 0; Mismatches 119; Indels
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Sequence 15342, Application US/09918995
Publication No. US20030073623A1
GENERAL INCORMATION:
APPLICANT: Hyesq. Inc.
ITILE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
ITILE OF INVENTION: PROM VARIOUS cDNA LIBRARIES
ITILE OF INVENTION: PROM VARIOUS cDNA LIBRARIES
ITILE OF INVENTION: 109/09/918,995
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: Fastered for Windows Version 3.0
SEQ ID NO 15342 | FEATURE: | NAME/KEY: misc_feature | LOCATION: (1)...(465) | OTHER INFORMATION: n = A,T,C or G TYPE: DNA ORGANISM: Homo sapiens

Gapa ; 0 Length 465; Query Match
9.3%; Score 31.4; DB 10; Length
Best Local Similarity 58.9%; Pred. No. 0.69;
Matches 53; Conservative 0; Mismatches 37; Indels

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dacadedraacageriegricaagaegereae 212 62 GACAGCTCGINTCATGATCGACTCGGACCC 91

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US-10-044-090-506/c

Sequence 506, Application US/10044090
Publication No. US2020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENER DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REPERENCE: PA.0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT PILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGRAM
SEQ ID NO 506
LENGTH: 1651
TYPE: DNA

NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No. US20020137081A1 403121.11 US-10-044-090-506 ORGANISM: Homo sapiens

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Gaps ô Query Match 9.3%; Score 31.4; DB 14; Length 1651; Best Local Similarity 50.7%; Pred. No. 1.2; Matches 68; Conservative 0; Mismatches 66; Indels 0;

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셤 ò Search completed: June 4, 2004, 16:50:42 Job time: 294 secs

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Sequence 14, Appl
Sequence 1843, Ap
Sequence 5514, Ap
Sequence 5584, Ap
Sequence 1639, Ap
Sequence 18442, Ap
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Sequence 1866, Ap
Sequence 1659, Ap
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4709, Ap
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Sequence 1, Appli Sequence 1, Appli Sequence 1250, A Sequence 1250, A Sequence 2626, Ap Sequence 2626, Ap Sequence 2626, Ap Sequence 2626, Ap Sequence 3513, Ap Sequence 7023, Ap Sequence 1269, Ap Sequence 2407, Ap Sequence 2407, Ap Sequence 1185, Ap Sequence 1185, Ap Sequence 1185, Ap Sequence 13184, Ap Sequence 131

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Matches 22; Conservative 0; Misma Qy 11 TTTTCTATGCTCTCCTGCTGG 32	TITLE OF INVENTION: Acyl-CoA.cholester TITLE OF INVENTION: Acyl-CoA.cholester; TITLE OF INVENTION: Acyl-CoA.cholester; ELLB CP. INVENTION: Acyl-CoA.cholester; CURRENT PERENCOE: 170-5/100/00 CURRENT FILING DATE: 1999-06-04 PRIOR APPLICATION NUMBER: 60/088,143 PRIOR APPLICATION NUMBER: 60/108,389 PRIOR FILING DATE: 1998-11-12 NUMBER OF SEQ ID NOS: 46; SOFTWARE: Patentin Ver. 2.1; SEO ID NO 14	TYPE: DENGTH: TYPE: DEORGANISH FEATURE NAME/KEN LOCATION OTHER IN	Query Match Best Local Similarity 100.0%; Pred. N Matches 20; Conservative 0; Misma Qy 22 CTCCTGCTGGCGCTGATGG 41 Db 524 CTCCTGCTGGCGCTGATGG 543	RESULT 3 US-09-165-042-2 Sequence 2, Application US/09165042 Fatent No. 610007 GENERAL INFORMATION: APPLICANT: Sturley, Stephen L. TITLE OF INVENTION: ISOLATION OF A GENERAL TITLE OF INVENTION: SCLATTON OF A GENERAL TITLE OF INVENTION: ACYLTRANSFERASE CURRENT APPLICATION: ACYLTRANSFERASE CURRENT APPLICATION: ACYLTRANSFERASE CURRENT APPLICATION: ACYLTRANSFERASE NUMBER OF SEQ ID NOS: 32 NUMBER OF SEQ ID NOS: 32 ISOFTWARE: PatentIn Ver. 2.0 IENGTH: 1976	; TYPE: DNA ; ORGANISM: Yeast US-09-165-042-2 Query Match Best Local Similarity 100.0%; Fred. N Matches 20; Conservative 0; Misma Qy 22 CTCCCTGCTGGCGCTGATGG 41 Db 823 CTCCCTGCTGGCGCTGATGG 842
977 13 3.9 1164 4 US-09-252-991A-5240 Sequence 5240, Ap 978 13 3.9 1167 4 US-09-489-039A-5703 Sequence 5703, Ap 978 13 3.9 1173 4 US-09-536-382A-14 Sequence 3422, Ap 981 13 3.9 1173 4 US-09-252-991A-3422 Sequence 11771, A 982 13 3.9 1190 4 US-09-252-991A-11771 Sequence 4952, Ap 984 13 3.9 1190 4 US-09-252-991A-1451 Sequence 1, Appli 985 13 3.9 1194 4 US-09-252-991A-1451 Sequence 14514, A 986 13 3.9 1194 4 US-09-252-991A-1379 Sequence 7454, Ap 987 13 3.9 1194 4 US-09-252-991A-1379 Sequence 13679, A 988 13 3.9 1206 4 US-09-252-991A-13679 Sequence 160, App 989 13 3.9 1206 4 US-09-252-991A-9058 Sequence 2124, Ap 989 13 3.9 1206 4 US-09-252-991A-9058 Sequence 2124, Ap 990 13 3.9 1206 4 US-09-252-991A-9058 Sequence 5058, Ap	991 13 3.9 1209 4 0S-09-489-039A-354 Sequence 992 13 3.9 1215 4 0S-09-489-039A-1776 Sequence 993 13 3.9 1215 4 0S-09-489-039A-1776 Sequence 994 13 3.9 1215 4 0S-09-489-039A-4945 Sequence 995 13 3.9 1218 4 0S-09-489-039A-494 Sequence 996 13 3.9 1218 4 0S-09-489-039A-403 Sequence 997 13 3.9 1221 4 0S-09-252-991A-13701 Sequence 998 13 3.9 1245 4 0S-09-252-991A-10292 Sequence 999 13 3.9 1246 4 0S-09-252-991A-7361 Sequence 1000 13 3.9 1251 4 0S-09-252-991A-7361 Sequence	RESULT 1 US-09-620-312D-625 Sequence 625, Application US/09620312D Partent No. 6569662 GRNERAL INFORMATION:) APPLICANT: Tang, Y. Tom) APPLICANT: Liu, Chenghua) APPLICANT: Bang, Jie APPLICANT: Ren, Feiyan) APPLICANT: Chen, Rui-hong APPLICANT: Chen, Rui-hong) APPLICANT: Wehrman, Tom) APPLICANT: Wehrman, Tom	## APPLICANT: Yang, Yonghong ## APPLICANT: Ano, Jian-Rui ## APPLICANT: Ano, Ping ## APPLICANT: Ano, Ping ## APPLICANT: Ma, Yunqing ## APPLICANT: Mang, Unrui ## APPLICANT: Wang, Zhiwei ## APPLICANT: John Tillinghast ## APPLICANT: John Tillinghast ## APPLICANT: John Tillinghast ## APPLICANT: John Tillinghast ## APPLICANT: Drmanac, Raddep T. ## APPLICANT: John Tillinghast ## APPLICANT: John Tillinghast ## APPLICANT: No. 656962e1 Nucleic Acids and ## TITLE OF INVENTION: PolyPeptides ## TITLE OF INVENTION: PolyPeptides ## TITLE OF INVENTION NUMBER: US/09/620,312D ## CURRENT APPLICATION NUMBER: US/09/622,317 ## PRIOR FILING DATE: 2000-04-25 ## PRIOR FILING DATE: 2000-01-21 ## PRIOR FILING DATE: 2000-01-21	NUMBER OF SEQ ID NOS: 1105 SOFTWARE: Pt_Genes Version 1.0 SEQ ID NO 625 LENGTH: 1878 TENTER: DNA PEATURE: PEATURE: LOCATION: (945)(1229) US-09-620-312D-625 Query Match 6.5%; Score 22; DB 4; Length 1878; Best Local Similarity 100.0%; Pred. No. 0.0028;

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ist, Mike
lisky, Diane
lisky, Diane
liskon-Control Acyltransferase Related Nucleic
liskon-Control Sequences
7045/00/WO
NINDMERR: US/09/326,203A
NINDMERR: G0/088,143
1998-06-05
NUMBER: 60/088,143
1998-06-105
NUMBER: 60/088,143
1998-06-105
NUMBER: 60/088,143
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NUMBER: 60/088,143
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NUMBER: 60/088,143
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Peter
I SOLATION OF A GENE ENCODING DIACYLGLYCEROL
1 ACYLTRANSFERASE
75/56331
8 NUMBER: US/09/165,042
E: 1998-10-01
So: 32.0
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100.0%; Pred. No. 0.045;
ative 0; Mismatches 0; Indels
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on US/09326203A
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GGCGCTGATGG 543
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GGCGCTGATGG 842
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PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 5584 LENGTH: 2079
                                                                                              ; LENGTH: 2079
; TYPE: DNA
; ORGANISM: Beeudomonas aeruginosa
US-09-252-991A-5584
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION NUMBER: US/09/252,991A
CURRENT PILLING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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Sequence 5584, Application US/09252991A

Sequence 5581, Application US/09252991A

Patent No. 6551795

Patent No. 6551795

Patent No. 6551795

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18
                                      Sequence 1843, Application US/09489039A

Paleant No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Ereton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-29
PRIOR FLIING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 1843
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100.0%; Pred. No. 2.8;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5614
                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Klebsiella pneumoniae
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Best Local Similarity 100.1
Matches 17; Conservative
                    US-09-489-039A-1843
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RESULT 8

US-09-489-039A-887/C

Sequence 847, Application US/09489039A

Patent No. 661836

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUMBER: US/09/489, 039A

TITLE OF PAPILCATION NUMBER: US/09/489, 039A

CURRENT APPLICATION NUMBER: US/09/489, 039A

CURRENT PILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 390
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELIGIONED PRINTING PRINTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELIGIONED PRINTING PARTICINATION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTING FILES REFERENCE: 107196.136
CURRENT PRILICATION NUMBER: US 60/074,788
PRIOR PRILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5645
LENGTH: 2436
Query Match 5.1%; Score 17; DB 4; Length 2079; Best Local Similarity 100.0%; Pred. No. 2.8; Matches 17; Conservative 0; Mismatches 0; Indels
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4.8%; Score 16; DB
Best Local Similarity 100.0%; Pred. No. 9.9
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                 US-09-252-991A-5645
; Sequence 5645, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
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Sequence 4989, Application US/09489039A

F Sequence 4989, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: GATY BRECOM et. al
APPLICANT: GATY BRECOMENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: FNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
FRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342

SRQ ID NO 4989
LENGTH: 960
TYPE: DNA
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US-09-489-039A-4386

i Sequence 4386, Application US/09489039A

i Sequence 4386, Application US/09489039A

patent No. 6610836

i GENERAL INFORMATION:

APPLICANT: CALY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT PILING DATE: 2000-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 771
                PATENT NO. 6610836
GENERAL INFORMATION:
APPLICANT: GATY BROWNER:
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 94
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Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Length 651;
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Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches
Sequence 94, Application US/09489039A
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                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 ccrecrececreare 228
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red. No. 10;
Mismatches 0; Indels
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4.8%; Score 16; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                             Sequence 10142, Application US/09621976
Fatent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET: 054FR2
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 18442
FERNION: SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
IOCATION: 47..274
NAME/KEY: sig_peptide
LOCATION: 47..124
CTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.4000009536743
US-09-621-976-1639
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ઠે 셤 RESULT 10 US-09-621-976-18442

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RESULT 11 US-09-489-039A-94

29 CTGGCGCTGATGGGAG 44

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TYPE: DNA
CORGANISM: Homo sapiens
US-09-621-976-18442

173 CCTGCTGGCGCTGATG 158

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25 CCTGCTGGCGCTGATG 40

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RESULT 14
US-09-543-691A-1655/c
is equance 1655, Application US/09543681A
is patent No. 6605709
igeneral NPORMATION:
APPLICANT GARY BRETON
it TILL OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
if TILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
if TILE OF INVENTION NUMBER: US 60/128,706
if PRIOR FILING DATE: 1999-04-09
if NUMBER OF SEQ ID NOS: 8344
if LENGTH: 1020
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US-09-489-039A-754
Sequence 754, Application US/09489039A
; Sequence 754, Application US/09489039A
; Sequence 754, Application US/09489039A
; Sequence 754, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
    APPLICANT: Gary Breton et. al
    APPLICANT: GARY Breton et. al
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
; CURRENT PAPLICATION NUMBER: US 60/117,747
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILLING DATE: 1999-01-29
; SEQ ID NO 754
; LENGTH: 1023
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Best Local Similarity 100.0%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 0; Indels
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4.8%; Score 16; DB 4; Length 1023;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 0; Indel8
                                                                                        Query Match 4.8%; Score 16; DB 4; Length 960;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 0; Indels
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Job time : 83 secs
; ORGANISM: Klebsiella pneumoniae US-09-489-039A-4989
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; ORGANISM: Klebsiella pneumoniae
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170 CCCTGCTGGCGCTGAT 185
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; ORGANISM: Proteus mirabilis
US-09-543-681A-1655
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                                                                      June 4, 2004, 17:48:00 ; Search time 292 Seconds (without alignments) 5249.420 Million cell updates/sec
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US-10-176-984-353 US-10-179-508-353 US-10-179-512-353 US-10-179-515-353 US-10-173-692-353	0-015-392A-323	0-017-306A-323 0-173-702-353)-173-703-353 -173-704-353	0-174-574-353	J-176-486-353 J-176-490-252	0-176-752-353	0-176-981-353	J-176-983-353 -176-988-353	0-179-517-353	0-179-521-353	0-017-867A-323	J-012-084A-323 J-202-475-353	0-013-909A-323	0-015-671A-323	J-015-610A-323	J-012-15/A-323	0-012-754A-323	0-013-910A-323	0-013-911A-323	J-015-912A-525 J-015-6538-303	0-012-101B-323	0-015-480A-323	J-015-715A-323 J-012-2378-323	0-013-906A-323	0-015-388A-323	0-012-753A-323 0-015-385A-323	0-007-236A-323	0-015-389A-323	0-013-915A-323	0-015-394A-323)-195-887-353 -106-003-353	0-179-509-353	0-194-486-353	J-195-900-353 J-198-759-353	0-205-506-353)-179-523-353 -100-463-363	0-202-471-353	0-207-915-353	J-015-390A-323 J-006-746A-323	0-011-795A-323	0-012-231A-323	- Ly/~/UY-553 - 206-916-353	8-09-770-445-48	3-369-493-24534	J-369-493-46622 J-305-700-3474	0-027-632-254555	0-027-632-254555	J-424-599-142420 J-276-774-1020	J-424-599-82767	S-09-938-842A-1804
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Sequence 116552, Sequence 12, Appl Sequence 11, Appl	1292,	Sequence 212, App Sequence 241, App	Sequence 241, App	717,		Sequence 358, App	13, A	Sequence 1565, Ap	Sequence 27209, A	Sequence 2036, Ap	Seguence 730, App	Sequence 1980, Ap	Sequence 172, App	Sequence 95, Appl	'n		Sequence 1079, Ap	2287,	'n	2287,				(4	1321	37, 7	190	34, 7	742,		82, 1		Sequence 1831, Ap	
US-10-424-599-116552 US-10-300-453A-12 US-10-300-453A-11		6 US-10-085-117-212 US-08-781-986A-241	3 US-10-329-624-241		US-10-060-036-15		5 US-10-262-538-13	₽		6 US-10-062-674-2036		6 US-10-062-674-1980	US-09-969-347-172	US-09-971-392-95	3 US-10-282-122A-33353	US-09-764-847-1079	S US-10-092-154-1079	US-09-764-869-2287	5 US-10-091-504-2287	-577-22	5 US-10-388-934-556		5 US-10-085-117-211	2 US-09-997-722-286	3 US-10-087-192-1321	5 US-10-085-117-37	3 US-10-087-192-190	2 US-10-052-482-34	3 US-10-087-192-742	3 US-10-087-192-562	2 US-10-052-482-82	-09-847	3 US-10-087-192-1831	
4.5 3832 13 4.5 3942 15 4.5 3981 18	4080	4.5 4236 16 4.5 5000 8	5000	H	5177 1	H	ਜ	5588 9	Н	5763 1	Н	Н	4.5 6571 9	4.5 6577 10	4.5 8646 13	4.5 10923 9	4.5 10923 1	4.5 18036 9	4.5 18036 1	4.5 18036 10	4.5 25759 10		m	4.5 38764 13	4.5 38977 13	4.	4.5 54200 1	4.5 57763 13	4.5 78268 13	4.5 85859 1	4.5 87878 13	5184 1	4.5 126413 13	
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ALIGNMENTS

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RESULT 1
US.10-355-716-74
US.10-355-716-74
US.10-355-716-74
Sequence 74, Application US/1035516
Publication No. US20030216339A1
GENERAL INFORMATION:
MAX PAPLICANT: Cynader, Max
TITLE OF INVENTION: GENER SEQUENCES ASSOCIATED WITH NEURAL
PLASTICITY AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 132
CORRESPONDENCES: 132
CORRESPONDENCES: 134
ADDRESSEE: Seed Intellectual Property Law Group FLLC
STREET: 701 Fifth Avenue, Suite 6300
COUNTRY: USA
ZITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 9310-4-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: PACHILIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/355,716
FILLING DATE: 31-3n-2003
CLASSIFICATION NUMBER: US/09/301,507
FILLING DATE: 28-Apr-1999
ATTORNEY/AGENT INPORMATION:
NAME: POTLEY, Jane E. R.
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCTGAGNTTCCAGAGGGNCCTGGTCGTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 CCATCGCCTAGCAGGGTTCAAGNAAAGGGGCCCGCNCATGGCAGTCCTTGGNCAGNAAAA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGACAGCTCGINTCATGATCGACTCGGACCCTCTGCGNCTGCATGAGGCACCACTATGTT
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US-10-76
Sequence 76, Application US/10355716
Sequence 76, Application US/10355716
Publication No. US20030216339A1
GENERAL INFORMATION:
Presed, Shiv
TITLE OF INVENTION: GENE SEQUENCES ASSOCIATED WITH NEURAL
TITLE OF INVENTION: GENE SEQUENCES ASSOCIATED WITH NEURAL
CORRESPONDENCE 3.132
CORRESPONDENCE 3.132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible OPERAINE STEM: PC-DOS/MS-DOS
SOFTWARRE: PARAININ RELABER
CURRENT APPLICATION DARK:
COMPUTER READABLE PORTION DARK:
COMPUTER PRESENTED THE PORTION DARK:
COMPUTER PROSENTED THE PORTI
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REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 230018.401C1

TELECOMUNICATION INFORMATION:
TELEPRAK: (206) 622-6331
TELEPRAK: (206) 682-6331
TELEPRAK: (206) 682-6331
TELEPRAK: (206) 74:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
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100.0%; Score 336; DB 16;
Best Local Similarity 100.0%; Pred. No. 3.3e-187;
Matches 336; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 ANGGANTIGGNCCCAACCCCNTIGGITCCCAACCCA 336
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APPLICATION NUMBER: US/09/301,507
FILING DATE: 28-Apr-1999
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/355,716
FILING DATE: 31-Jan-2003
CLASSIFICATION: <Unknown>
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TYPE: DNA ORGANISM: Homo sapiens
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US-10-198-846-1775
Sequence 1775, Application US/10198846
Fublication No. US200099974A1
GENERAL INFORMATION:
APPLICANT: Lillib., James
APPLICANT: Winy Youzhen
TILLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TILLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TILLE OF INVENTION: THERAPY OF BREAST CANCER
FILLE REFERENCE: MI - 049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: 60/306,220
PRIOR FILLING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOUTHARE: FREESE FREES
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6.5%; Score 22; DB 15; Length 412;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 22; Conservative 0; Mismatches 0; Indels
NAME: Potter, Jane B. R.
REGISTRATION NUMBER: 33, 332
REFERENCE/DOCKET NUMBER: 230018,401C1
TELEPHONICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY, linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 76: US-10-355-716-76
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US-10-198-846-8657
; Sequence 8657, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 rrirchardcrcrcccrdcrdg 80
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; NAME/KEY: misc feature

; LOCATION: 3, 203, 293, 343, 398

; OTHER INFORMATION: n = A,T,C or G

US-10-198-846-1775
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ORGANISM: Homo sapiens
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APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND WETHODS
TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REPERENCE: MRI-049
CURRENT APPLICATION NUMBER: 105/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR PILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE PESTSEQ for Windows Version 4.0
SEQ ID NO 8657
LENGTH: 455
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APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Wang, Junging
APPLICANT: Wang, Zhiwei
APPLICANT: Tillinghase, John
APPLICANT: PARCHON: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784C1P2B;
CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 1104
SOPTWARE: PL. FL. genes Version 1.0
SEQ ID NO 625
LENGTH: 1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.5%; Score 22; DB 15; Length 455; Best Local Similarity 100.0%; Pred. No. 0.025; Matches 22; Conservative 0; Mismatches 0; Indels
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Publication No. US20030104529A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 TTTTCTATGCTCTCCCTGCTGG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                          | FRATURE: | NAME/KEY: misc feature | LOCATION: 2, 7, 404, 454 | COTHER INFORMATION: n = A,T,C or G US-10-198-846-8657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Annug, Jie
APPLICANT: Chang, Jie
APPLICANT: Chen, Felyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (945)..(1229)
US-10-037-270-625
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ORGANISM: Homo sapiens
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Query Match 6.0%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 0.3 Matches 20; Conservative 0; Mismatches
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; ORGANISM: Homo sapien
US-09-867-701-5894
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US-09-867-701-2415
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| Publication No. US20030099974A1
| GENERAL INFORMATION:
| APPLICANT: A. Lillie, James
| APPLICANT: A. Lillie, James
| APPLICANT: A. Lillie, James
| APPLICANT: Mang, YouZhen
| APPLICANT: Wang, YouZhen
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
| TITLE OF INVENTION: THERAPY OF BREAST CANCER
| TITLE OF INVENTION: THERAPY OF BREAST CANCER
| TITLE OF INVENTION: THERAPY OF BREAST CANCER
| CURRENT FILING DATE: 2002-07-18
| FRICE REFERENCE: MRI-049
| CURRENT FILING DATE: 2002-07-18
| FRICE PRICE THE CONTINUENT ON THE CONTINUE
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US-10-117-722-625

Squence 625, Application US/1011722

Publication No. US20030219744A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Asund; Vinod

APPLICANT: Anng, V. Tom

TITLE OF INVENTION: No. US20030219744A1e1 Nucleic Acids and

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 784CIPSER: US/10/117,722

CURRENT APPLICATION NUMBER: 09/520,312

PRIOR FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-01-21

NUMBER: OF SEQ ID NOS: 1104

SEQ ID NO 625

LENGTHARE: PLEMENT AND NUMBER: OF SEQ ID NO 625

LENGTHARE: NUMBER: OF SEQ ID NOS: 1104

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Query Match 6.5%; Score 22; DB 15; Length 1878; Best Local Similarity 100.0%; Pred. No. 0.024; Matches 22; Conservative 0; Mismatches 0; Indels (
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; NAME/KEY: CDS
; LOCATION: (945)..(1229)
US-10-117-722-625
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ORGANISM: Homo sapiens
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US-10-198-846-11013
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LENGTH: 2061
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JOCATION: 18.25, 21.831, 1832, 1833, 1834, 1835, 1836, 1837, 1838, 160CATION: 18.26, 1840, 1841, 1842, 1844, 1845, 1846, 1847, 1848, 160CATION: 1839, 1840, 1841, 1842, 1844, 1845, 1846, 1847, 1848, 160CATION: 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2047, 2047, 2049, 2047, 2048, 2045, 2047, 2047, 2048, 2048, 2047, 2047, 2048, 2048, 2047, 2047, 2048, 2048, 2048, 2047, 2048, 2050, 2051, 2051, 2051, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2051, 2051, 2053, 2054, 2055, 2056, 2057, 20510, 2088, 2059, 2060, 2061
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US-09-867-701-5894

Sequence 5894, Application US/09867701

Patent No. US20020132237A1

Fatent No. US20020132237A1

Fatent No. US2002013237A1

APPLICANT: Aglate, Paul A.

APPLICANT: Aglate, Paul A.

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AUDIGNOSIS OF OVARIAN CANCER

FILE REPRENENCE 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5894
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| Patent No. US20020132237A1
| GENERAL INFORMATION:
| APPLICANT: Aglate, Paul A. |
| APPLICANT: Harlocker, Susan L. |
| APPLICANT: Harlocker, Susan L. |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: And DIAGNOSIS OF OVARIAN CANCER |
| TITLE OF INVENTION: And DIAGNOSIS OF OVARIAN CANCER |
| CURRENT FILLING DATE: 2001-05-29 |
| WUMBER OF SEQ ID NOS: 10912 |
| SOFTHARE: PastSEQ for Windows Version 4.0 |
| SEQ ID NO 2415 |
| LENGTH: 457 |
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0.38;
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                                                                                                                                            Query Match 6.0%; Score 20; DB 9; Length 457; Best Local Similarity 100.0%; Pred. No. 0.38; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: PATESE, NODERT V.
APPLICANT: Cases, Sylvaine
APPLICANT: Cases, Sylvaine
APPLICANT: Smith, Steven
TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
CURRENT APPLICATION NUMBER: US/10/040,315
PRIOR APPLICATION NUMBER: US/10/040,315
PRIOR APPLICATION NUMBER: 60/107,771
PRIOR APPLICATION NUMBER: 1998-11-09
PRIOR APPLICATION NUMBER: 09/103,754
PRIOR APPLICATION NUMBER: 09/103,754
PRIOR APPLICATION NUMBER: 09/103,754
PRIOR APPLICATION NUMBER: 09/339,472
PRIOR APPLICATION NUMBER: 1998-06-28
PRIOR APPLICATION NUMBER: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 1998-06-24
PRIOR PRIOR PRIOR OF SEQ ID NOS: 10
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO. 1
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APPLICANT: Parese, Robert V.
APPLICANT: Gases, Sylvaine
APPLICANT: Smith, Steven
APPLICANT: Smith, Steven
APPLICANT: Smith, Steven
TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
FILE REFERENCE: UCAL-105CIP2
CURRENT APPLICATION NUMBER: US/10/040,315A
CURRENT FILING DATE: 2001-10-29
PRIOR PILING DATE: 1998-11-09
PRIOR PILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: PCT/US98/17883
PRIOR APPLICATION NUMBER: 09/103,754
PRIOR PILING DATE: 1998-06-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 crecerecreececreares 292
; NAME/KEY: misc_feature
; LOCATION: (1)...(457)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-2415
                                                                                                                                                                                                                                                                     26 CTGCTGGCGCTGATGGGAGA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10273438 Publication No. US20030072757A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: homo sapiens
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PRICE APPLICATION NUMBER: 09(319)-472
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PRICE PRICE APPLICATION NUMBER: 09(319)-472
SUPPRICE TO THE APPLICATION NUMBER: 09(319)-66(23)
SUPPRICE TO THE APPLICATION NUMBER: 09(319)-66(23)
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SUPPRICE TO COMMENTARY 10(319)-66(23)
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SUPPRICE TO COMMENTARY 10(319)-66(23)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)-69(319)
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Page 12
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579 CTCCCTGCTGGCGCTGATGG 598
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Search completed: June
Job time : 296 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CRGANISM: Homo sapiens
FRATURE:
NAME/KRY: CDS
LOCATION: (1)...(1467)
OTHER INFORMATION: Homo sapiens diacylglycerol O-acyltransferase
CFER INFORMATION: homolog 1
US-10-278-733-2
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LOCATION: (1) ...(1467)

OTHER INFORMATION: Homo sapiens diacylglycerol O-acyltransferase

CTHER INFORMATION: homolog 1 (DGAT1), coding sequence
US-10-278-733-9
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US-10-2/9-34-9

US-10-2/9-34-9

Publication No. US20030100480A1

FENERAL INFORMATION:

APPLICANT: Smith, Steven

APPLICANT: Chen, Hubert

ITILE OF INVENTION: Methods and compositions for modulating

ITILE OF INVENTION: METHOD ADDRESSIVENCE: US/10/278,733

CURRENT APPLICATION NUMBER: US/10/278,733

CURRENT FILING DATE: 1999-06-23

FRIOR APPLICATION NUMBER: 09/339,472

PRIOR FILING DATE: 1999-06-23

FRIOR PELING DATE: 1999-06-23

FRIOR PELING DATE: 1998-10-29

FRIOR PELING DATE: 1998-10-29

FRIOR PELING DATE: 1998-06-24

FRIOR APPLICATION NUMBER: OS/103,754

FRIOR PELING DATE: 1998-06-24

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PRIOR APPLICATION NUMBER: 09/339,472
PRIOR APPLICATION NUMBER: 09/339,472
PRIOR PILLING DATE: 1999-06-23
PRIOR PLING DATE: 1998-10-09
PRIOR FILING DATE: 1998-11-09
PRIOR PILING DATE: 1998-11-09
PRIOR PILING DATE: 1998-128-28
PRIOR APPLICATION NUMBER: 09/103,754
PRIOR PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1467
TYPE: NNA
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ORGANISM: Homo sapiens
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Gaps

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Query Match 6.0%; Score 20; DB 15; Length 1467; Best Local Similarity 100.0%; Pred. No. 0.37; Matches 20; Conservative 0; Mismatches 0; Indels

22 CTCCCTGCTGGCGCTGATGG 41

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RESULT 15
US-10-157-855-14

i Sequence 14, Application US/10157855

i Sequence 14, Application No. US20020170091A1

i GENERAL INFORMATION:

i APPLICANT: Lassner, Michael W.

i TITLE OF INVENTION: Acrl CoA.Cholesterol Acyltransferase Related Nucleic

i TITLE OF INVENTION: Acrd Sequences

i TITLE OF INVENTION: Acrd Sequences

i TITLE OF INVENTION: Acrd Sequences

i TITLE OF INVENTION WIMBER: US/10/157,855

CURRENT APPLICATION NUMBER: 09/326,203

PRIOR FILING DATE: 1999-06-04

PRIOR PILING DATE: 1999-06-04

PRIOR FILING DATE: 1999-06-05

PRIOR FILING DATE: 1999-06-05

PRIOR FILING DATE: 1999-06-05

PRIOR FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 46

i SEQ ID NO 14

i ERWITH 1895

TURNEL 1895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
6.0%; Score 20; DB 14; Length 1895;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 20; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (209)
OTHER INFORMATION: n at position 209 is unknown US-10-157-855-14
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